

21

Figure 1

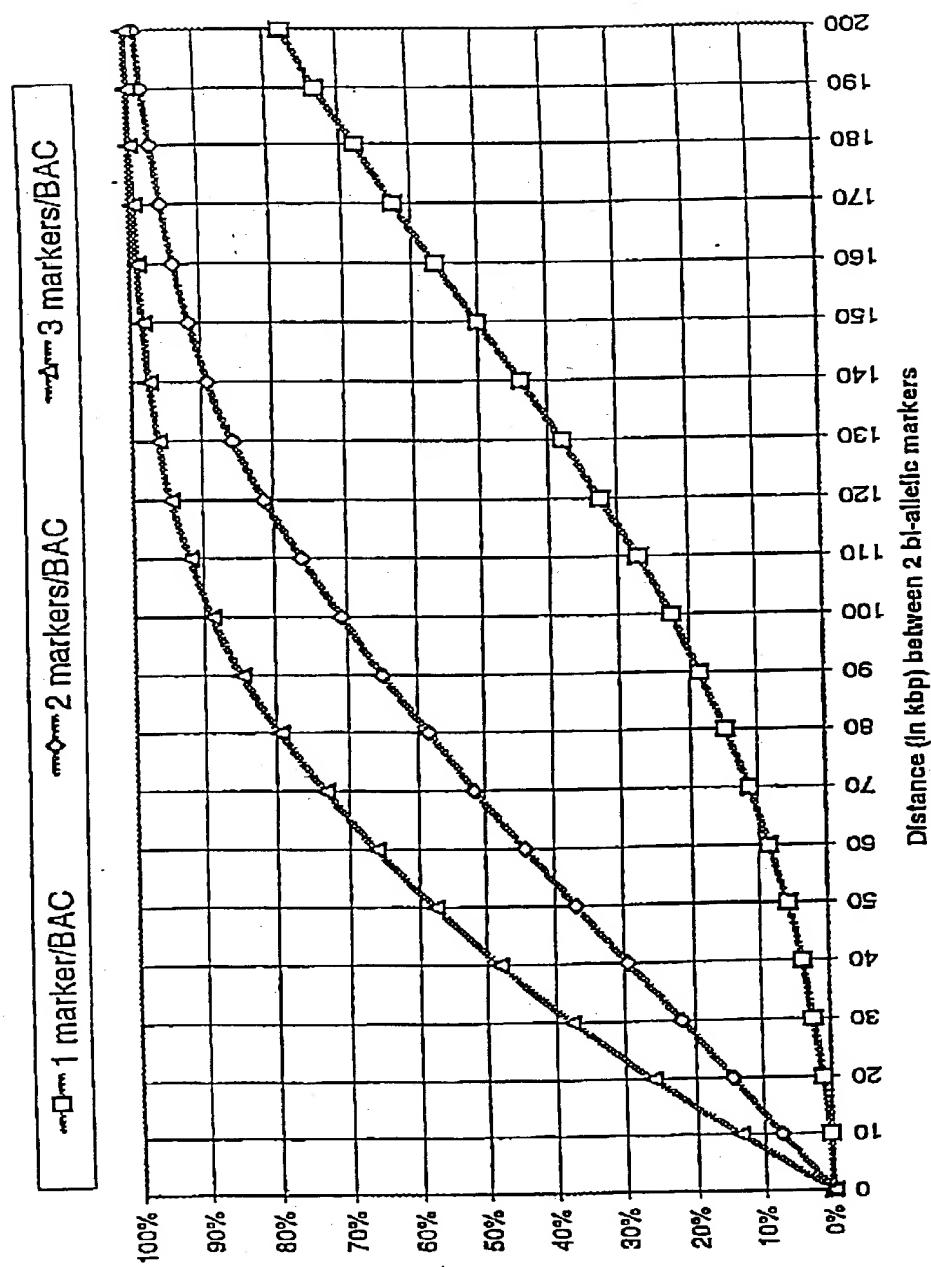
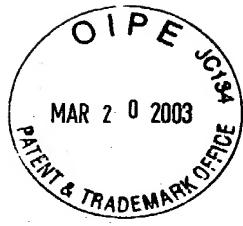


Figure 2A

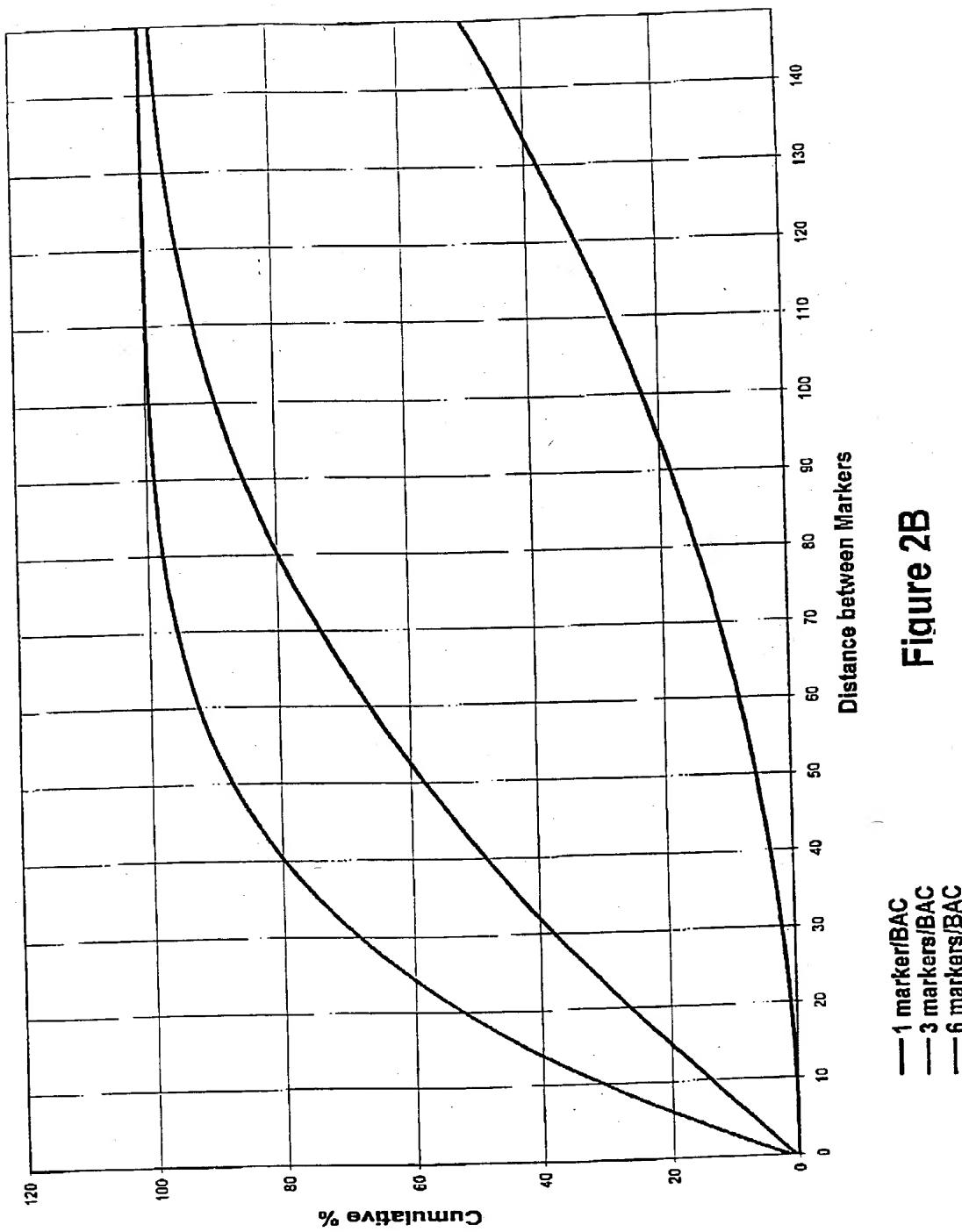


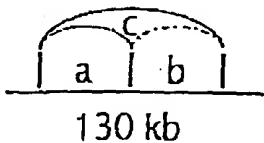
Figure 2B



00000000000000000000000000000000

## LD in a random French caucasian population

- 54 sized « random » BACs covering 8100 kb
- 213 SNP ; 2 to 6 / BAC, mean allele frequency = 0.3
- Order and distance unknown
- For 1 BAC :



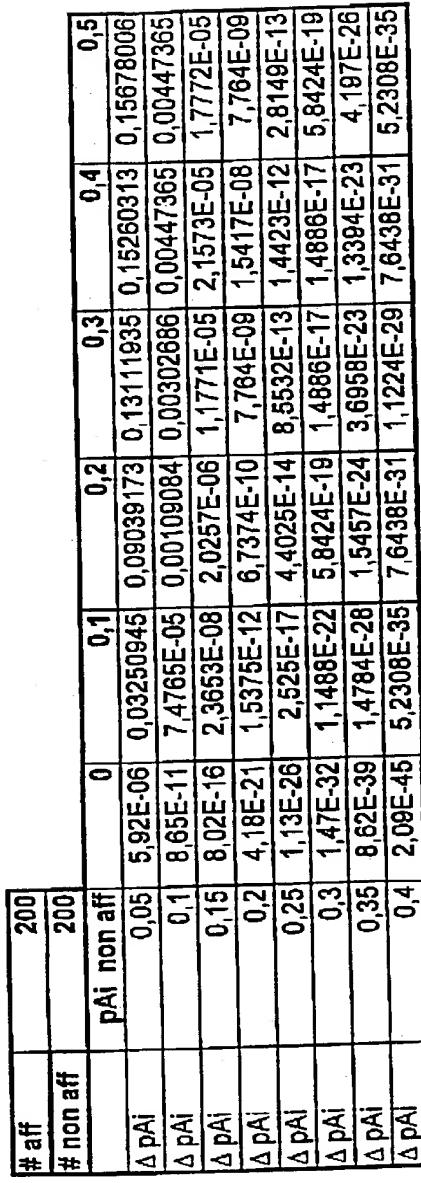
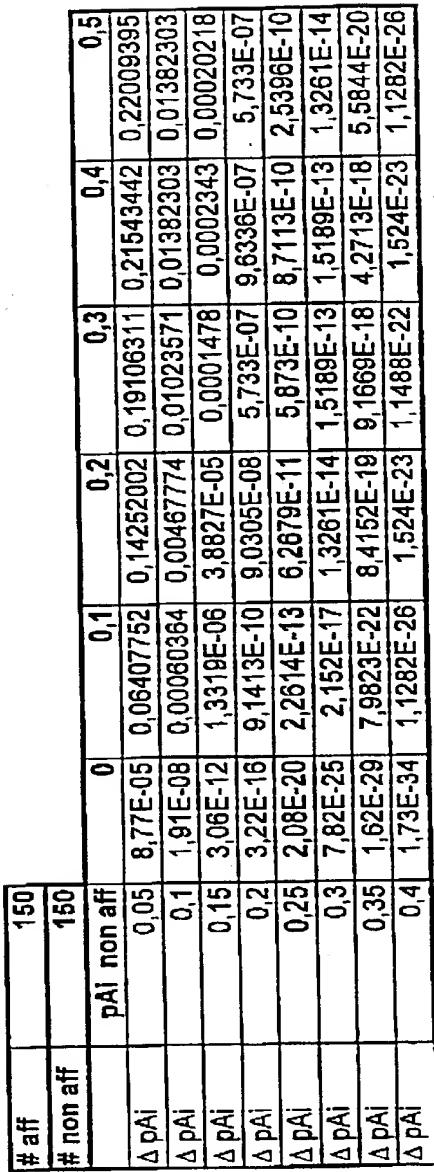
- \*  $\bar{m}$  intermarker distance :  $130/3 = 43$  kb
- \*  $\bar{m}$  LD strength estimate :  $m(a,b,c) = 0.51$

- For 54 BACs :
  - \*  $\bar{m}$  intermarker distance = 38 kb
  - \*  $\bar{m}$  LD strength estimate =  $0.63 \pm 0.05$   
(324 pairs)
- For 19 unlinked SNPs :  $m$  LD strength estimate =  $0.12 \pm 0.007$   
(171 pairs)

Figure 2c



p-VALUE DISTRIBUTION



# aff affected individuals  
# non aff non affected individuals  
pAi non aff allele frequency in non affected individuals  
△ pAi % Difference in allele frequency between affected and non-affected individuals

Figure 3 (I)



## D-VALUE DISTRIBUTION

# aff	500								
# non aff	500								
		PAI	non aff	0	0.1	0.2	0.3	0.4	0.5
Δ PAI	0.05	8E-13	0.00072323	0.00741965	0.0169842	0.02371865	0.02516449		
Δ PAI	0.1	1.07E-24	3.7948E-10	2.4176E-07	2.7579E-06	6.9679E-06	6.9679E-06		
Δ PAI	0.15	3.81E-37	1.0719E-18	5.8344E-14	4.2622E-12	1.8601E-11	1.1611E-11		
Δ PAI	0.2	2.96E-50	5.0895E-29	1.6881E-22	6.9321E-20	3.7441E-19	6.9321E-20		
Δ PAI	0.25	4.27E-64	7.2043E-41	7.7528E-33	1.184E-29	4.3462E-29	7.6438E-31		
Δ PAI	0.3	9.7E-79	3.9328E-54	6.3017E-45	1.9429E-41	1.9429E-41	6.3017E-45		
Δ PAI	0.35	2.91E-94	8.8513E-69	8.77879E-59	2.3478E-55	1.8839E-56	1.1206E-62		
Δ PAI	0.4	9.5E-111	7.7199E-85	1.8063E-74	1.4484E-71	1.8063E-74	7.7199E-85		

# aff	150							
# non aff		850						
		PAI	non aff	0	0.1	0.2	0.3	0.4
Δ PAI	0.05	2.16E-20	0.0099614	0.04896055	0.08358651	0.10417953	0.11025423	
Δ PAI	0.1	2.01E-39	5.571E-07	0.00010149	0.00058665	0.00119145	0.00139743	
Δ PAI	0.15	1.11E-58	2.7556E-13	8.462E-09	2.8851E-07	1.2395E-06	1.6229E-06	
Δ PAI	0.2	3.27E-78	2.1683E-21	3.2211E-14	1.1049E-11	1.111E-10	1.5638E-10	
Δ PAI	0.25	4.96E-98	4.4952E-31	6.5226E-21	3.1015E-17	2.5169E-16	1.1763E-15	
Δ PAI	0.3	3.7E-118	3.6987E-42	8.128E-29	6.9335E-24	5.4331E-22	6.5657E-22	
Δ PAI	0.35	1.4E-138	1.6797E-54	7.1058E-38	1.2938E-31	2.8415E-29	2.5869E-29	
Δ PAI	0.4	2.4E-159	5.4915E-68	4.8846E-48	2.1003E-40	1.33332E-37	6.8178E-38	

	# aff	# non aff	pA <sub>i</sub> non aff	Δ pA <sub>i</sub>
affected individuals				
non affected individuals				
allele frequency in non affected individuals				
% Difference in allele frequency				

Figure 3 (b)

## P-VALUE DISTRIBUTION

# aff	200								
# non aff	500								
		PAI	non aff	0	0,1	0,2	0,3	0,4	0,5
△ PAI	0,05	1,06E-12	0,00789803	0,03942384	0,06867566	0,08621572	0,09083704		
△ PAI	0,1	3,45E-24	4,4217E-07	5,6883E-05	0,00031976	0,0006363	0,00070881		
△ PAI	0,15	5,9E-36	4,3025E-13	3,3635E-09	9,2134E-08	3,319E-07	3,5871E-07		
△ PAI	0,2	4,73E-48	1,5566E-20	1,0346E-14	1,7218E-12	1,1512E-11	1,0047E-11		
△ PAI	0,25	1,67E-60	3,5436E-29	2,0473E-21	2,278E-18	1,1498E-17	1,3524E-17		
△ PAI	0,3	2,46E-73	7,2498E-39	3,0748E-29	2,0601E-25	3,4525E-24	7,4807E-25		
△ PAI	0,35	1,44E-86	1,6845E-49	3,9569E-38	1,4118E-33	2,6862E-32	1,4118E-33		
△ PAI	0,4	3,2E-100	5,3051E-61	4,7325E-48	7,1282E-43	1,0691E-41	7,2652E-44		

# aff	500								
# non aff	1000								
		pAi	non aff	0	0,1	0,2	0,3	0,4	0,5
$\Delta$ pAi	0,05	6,48E-24	5,7827E-05	0,00172627	0,00551541	0,00882876	0,00978249		
$\Delta$ pAi	0,1	6,53E-47	3,065E-14	1,0301E-09	4,3205E-08	1,8833E-07	2,2731E-07		
$\Delta$ pAi	0,15	1,2E-70	2,0716E-27	3,7441E-19	4,6626E-16	6,8719E-15	6,9719E-15		
$\Delta$ pAi	0,2	3,33E-95	1,1636E-43	1,6614E-31	8,5632E-27	4,1421E-25	1,9885E-25		
$\Delta$ pAi	0,25	1,2E-120	1,7683E-82	1,5328E-46	3,1722E-40	8,6765E-39	3,6071E-39		
$\Delta$ pAi	0,3	5,32E-147	1,526E-83	4,2697E-64	2,5988E-56	3,9328E-54	2,59888E-58		
$\Delta$ pAi	0,35	2,4E-174	1,184E-108	4,5658E-84	4,7426E-75	4,2624E-73	4,0958E-77		
$\Delta$ pAi	0,4	8,4E-203	1,0822E-131	2,137E-106	1,8014E-96	3,3252E-95	6,725E-102		

Figure 3 (iii)



ALLELIC ASSOCIATION  
3,000 MARKERS MAP

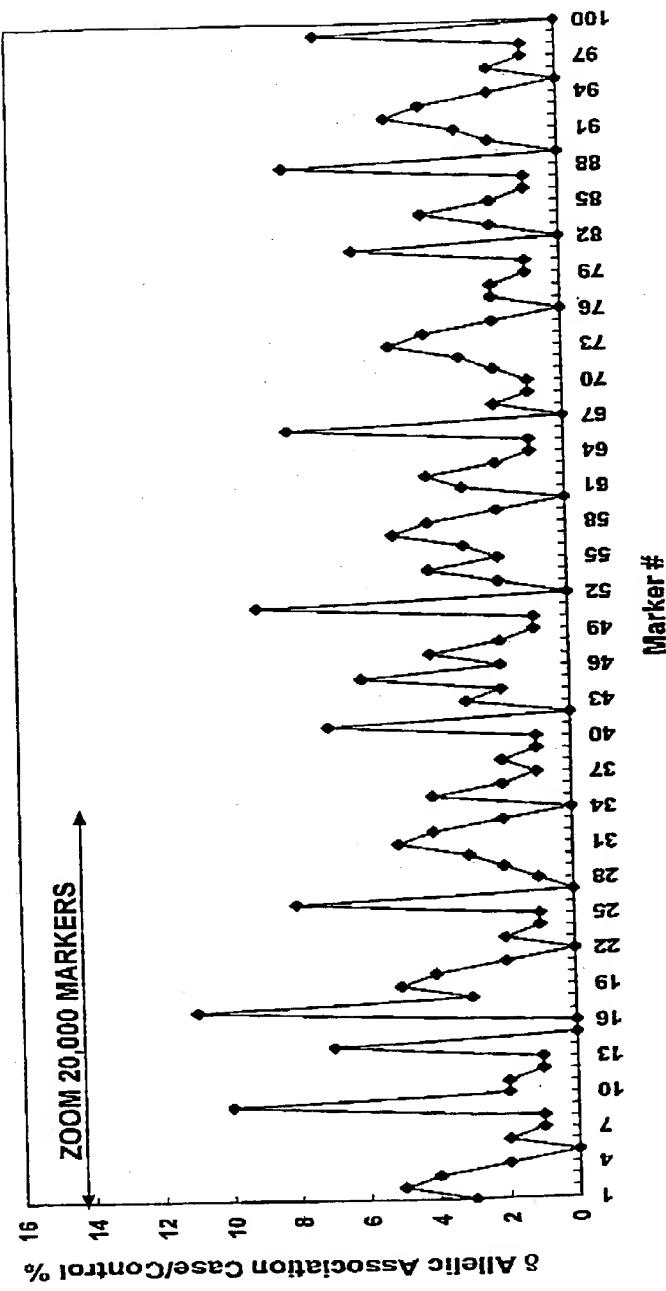


Figure 4



ALLELIC ASSOCIATION  
20,000 MARKERS MAP

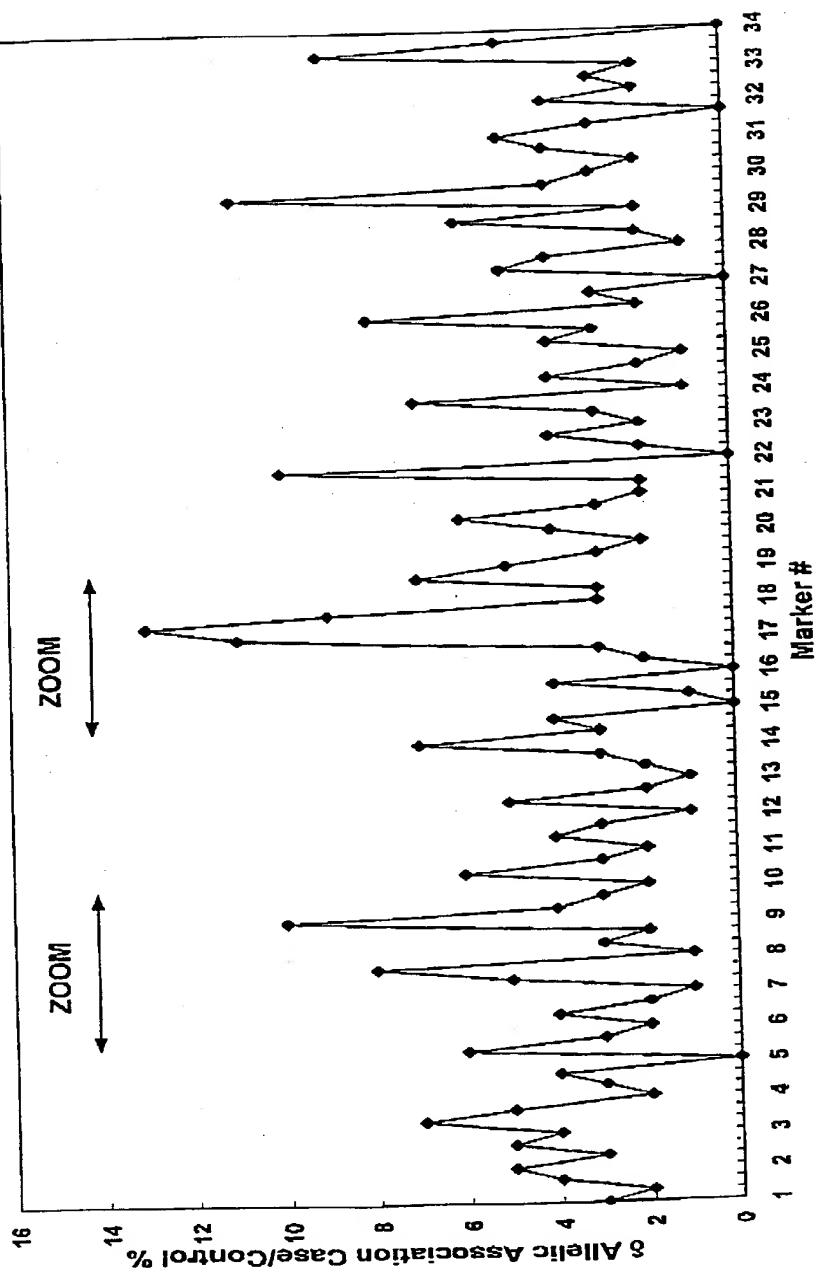


Figure 5

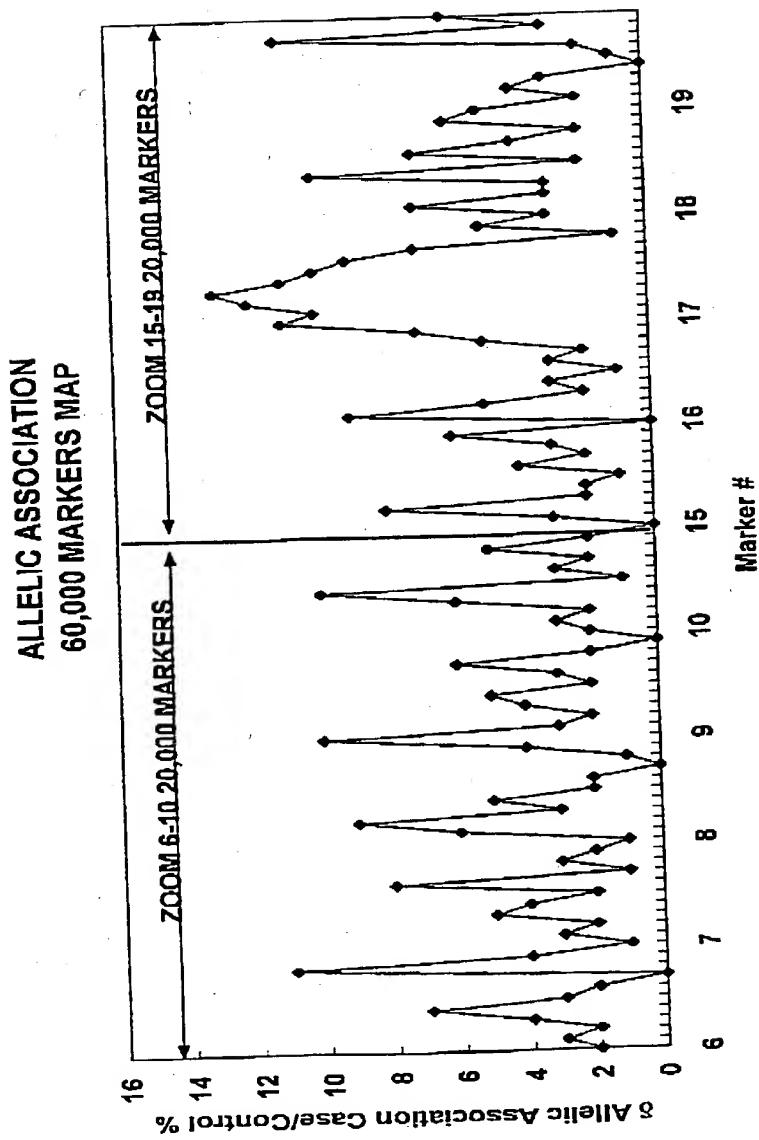


Figure 6



APO E REGION HAPLOTYPE FREQUENCY ANALYSIS

POPULATIONS	AD CASES (225)	AD CONTROLS (248)
-------------	----------------	-------------------

markers	99-366	99-344	99-359	99-355	haplotype frequencies	odds-ratio	P value
p value	3,01E-01	1,11E-01	6,63E-01	1,38E-01	cases controls		
haplotype 1	C	G			0,404 0,308	1,52	3,05E-03 ***
haplotype 2		G	A		0,203 0,165	1,29	1,24E-01 *
haplotype 3		G	G		0,375 0,306	1,36	2,83E-02 **
haplotype 4	C		A		0,264 0,209	1,36	5,95E-02 **
haplotype 5		G	A		0,116 0,071	1,70	1,64E-02 **
haplotype 6	C		A		0,15 0,129	1,19	3,59E-01 *
haplotype 7	T	A	G	G	0,225 0,122	2,09	4,76E-05 *****
haplotype 8	T	A	G	G	0,228 0,108	2,44	2,05E-06 *****

Figure 7



**APO E REGION HAPLOTYPE SIMULATION  
POPULATION: 225 CASES vs 248 CONTROLS**

Haplotype &	4 Markers				cases	controls	odds-ratio	pvalue
	99-344/435	99-366/274	99-359/303	99-355/219				
A	T	G	G	G	0,228	0,108	2,44	2,05E-06 *****

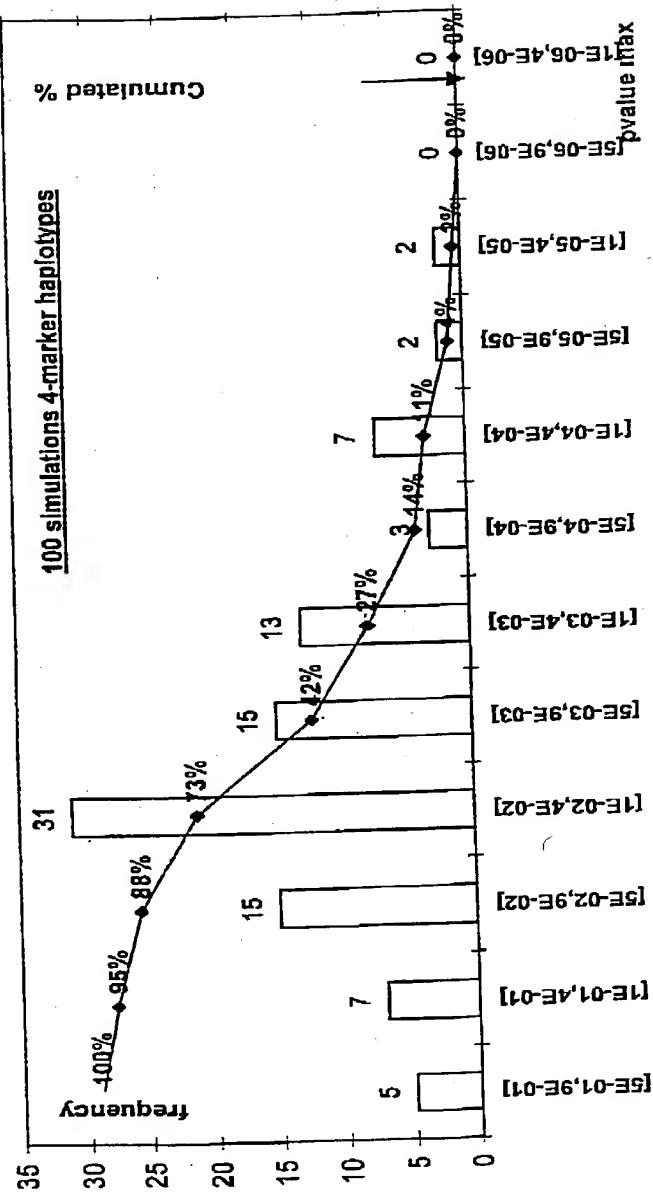


Figure 8

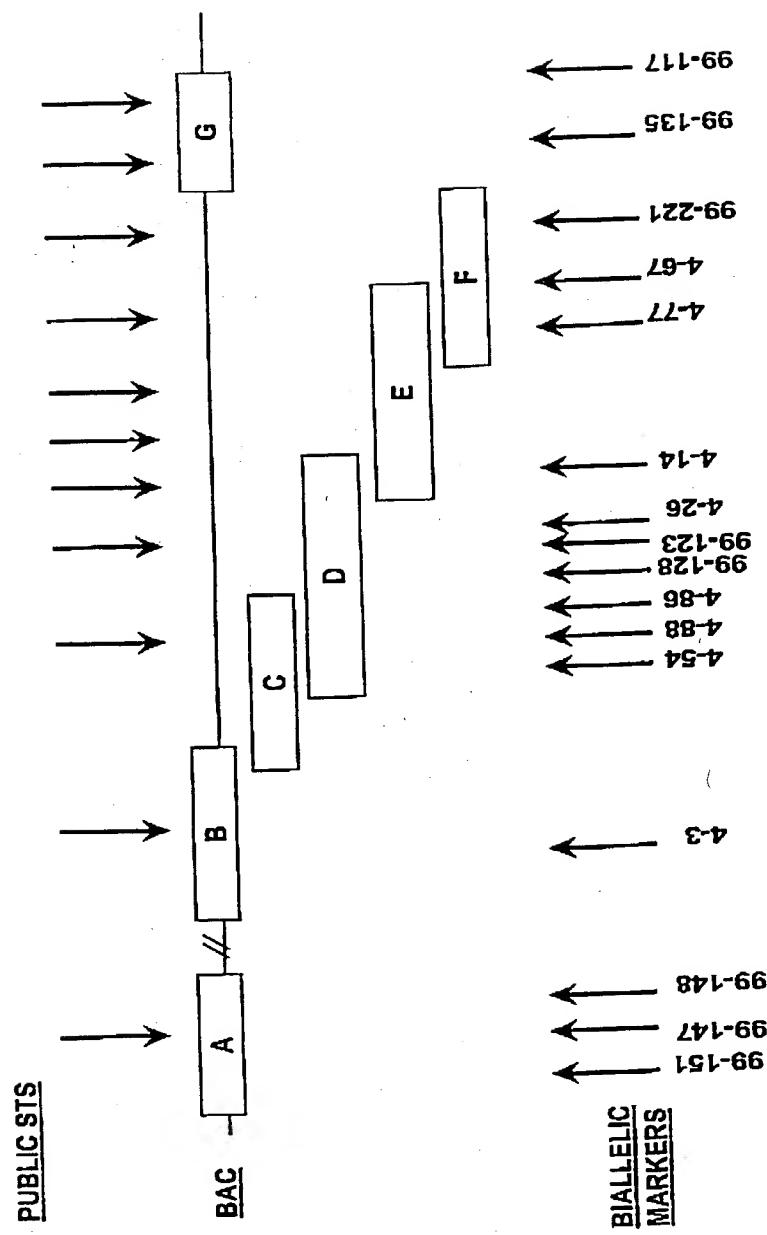


Figure 9



## PROSTATE CANCER ASSOCIATION STUDIES (FIRST SCREENING)

Population	PROSTATE CANCER	NON AFFECTED
Sample size	CASES = 112	CONTROLS=76
Population Characteristics	35 sporadic cases + 77 familial cases	> 65 years PSA<4

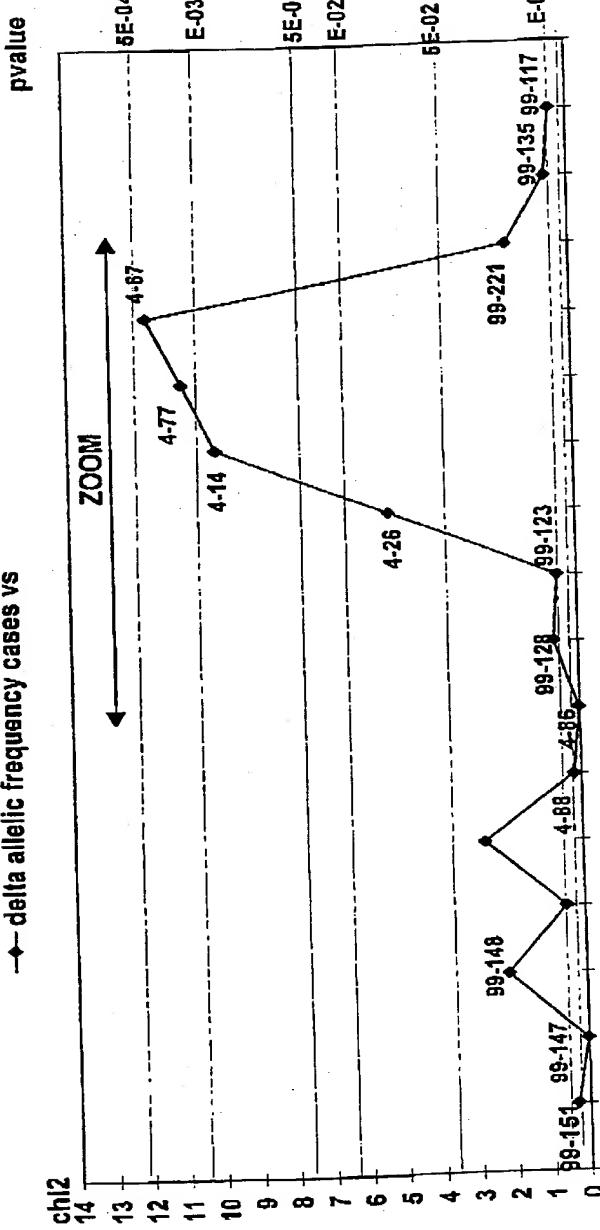


Figure 10



## PROSTATE CANCER ASSOCIATION STUDIES (ZOOM)

characteristics of populations	PROSTATE CANCER CASES (185)	NON-AFFECTED CONTROLS (104)
	47 sporadic cases + 138 familial cases	> 65 years PSA<4

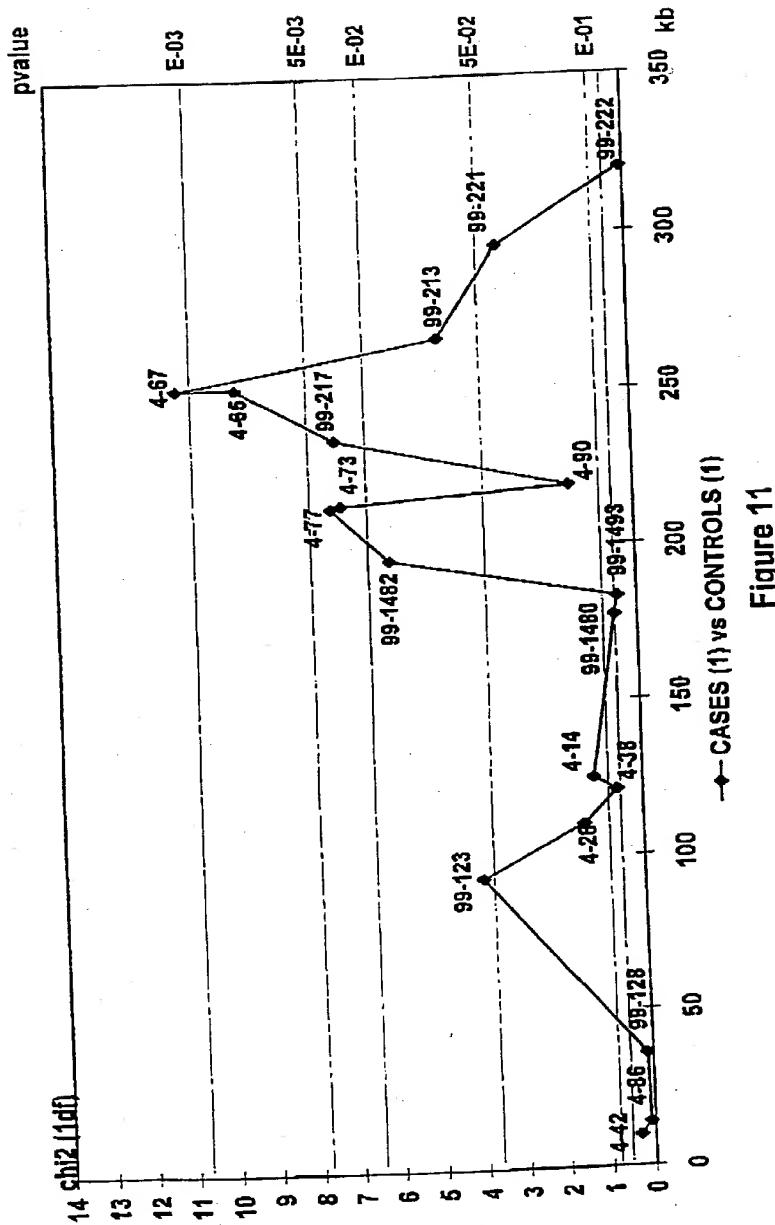


Figure 11

## PROSTATE CANCER HAPLOTYPE FREQUENCY ANALYSIS

	PROSTATE CANCER CASES (281)		NON-AFFECTED CONTROLS (130)	
	143 sporadic cases + 138 familial cases		> 65 years	PSA < 4
characteristics of populations				

markers	99-123	4-26	4-14	4-77	99-217	4-67	99-213	99-221	99-135	haplotype frequencies	relative risk	pvalue
bacs	H0287B09	B0189E08			B0463F01		B0725B12					
genes					PG1.....>							
p value	2,00E-01	1,00E-01	1,00E-01	2,00E-02	2,00E-02	6,00E-04	8,00E-02	7,00E-01	2,00E-01	cases	controls	
haplotype 8 >304kb<	C	A	C	G	T	T	C	A	A	0,075	0,018	4,42 9,00E-04 ***
haplotype 7 >286kb<		A	C	G	T	T	C	A	A	0,095	0,016	6,46 6,00E-05 ***
haplotype 6 <186kb>		A	C	G	T	T	C	A	A	0,116	0,019	6,78 1,00E-05 ***
haplotype 5 <171kb>		C	G	T	T	C	A	A	A	0,117	0,013	10,06 9,00E-07 ***
haplotype 4 <83kb>			G	T	T	C	A	A	A	0,117	0,025	5,17 2,00E-05 ***
haplotype 3.1 <54kb>				T	T	C	A	A	A	0,117	0,027	4,78 2,00E-05 ***
haplotype 3.2 <54kb>					G	T	T	C	C	0,222	0,108	2,33 4,00E-05 ***
haplotype 2.2 <39kb>					G	T	T	C	C	0,251	0,134	2,17 2,00E-04 ***
haplotype 2 <32kb>						T	T	C	C	0,226	0,112	2,32 1,00E-04 ***
haplotype 1.1 <17 kb>							T	T	T	0,256	0,148	2,01 3,00E-04 ***
haplotype 1.2 <15 kb>								T	C	0,233	0,129	2,05 6,00E-04 ***

Figure 12





### PROSTATE CANCER HAPLOTYPE SIMULATIONS (100 ITERATIONS)

markers	haplotype frequencies						cases	controls	relative risk	pvalue
	4-14	4-77	99-217	4-67	99-213	99-221				
haplotype	C	G	T	T	G	A	0,117	0,013	10,06	9,00E-07

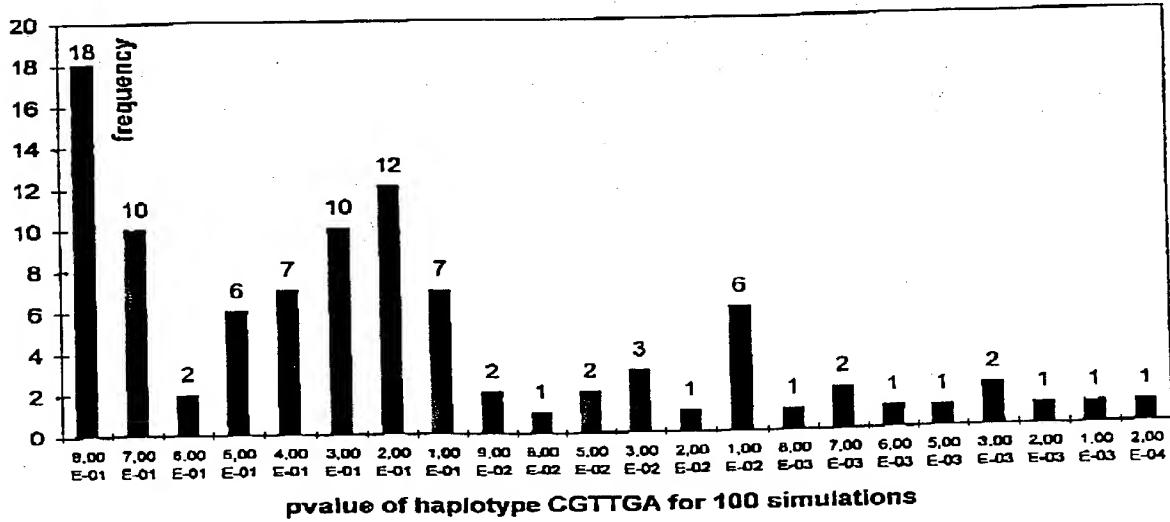
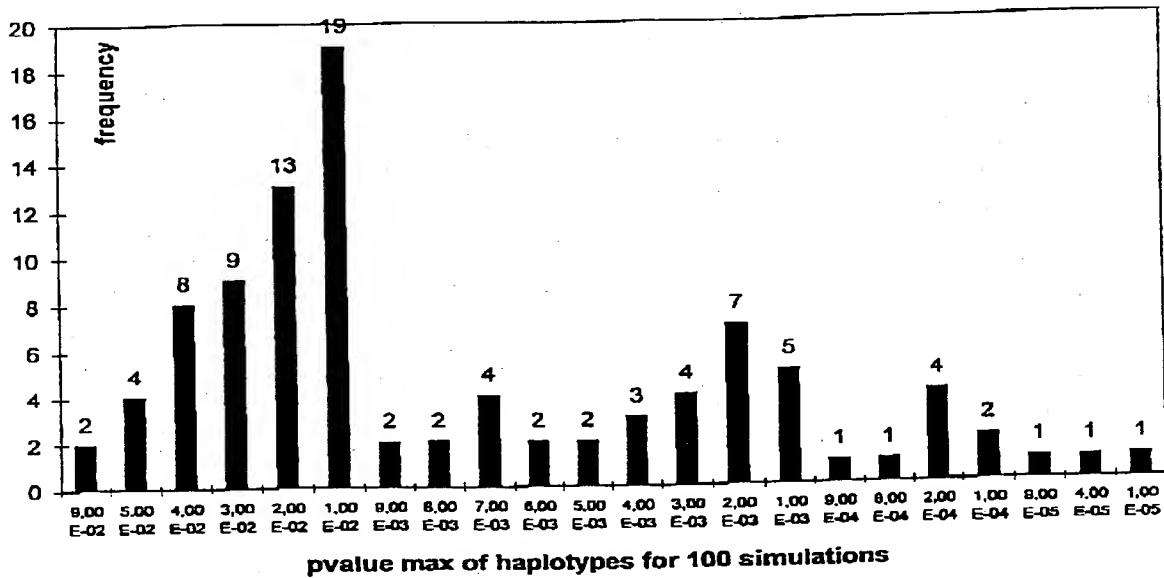


Figure 13



### AVERAGE LD PATTERN GENOMIC HETEROGENEITY

Recombination rate	Lower A	Higher B
Nb markers	89	69
All SNP	0.61 (749)	0.42 (1190)
Rare < 0.2	0.75	0.17
Rare vs rare	(65)	(158)
Frequent > 0.2	0.51	0.49
Frequent vs frequent	(410)	(544)
Rare vs frequent	0.72 (274)	0.41 (488)

FIGURE 14



### Exonic/nonexonic LD

	Nb pairs	Average intermarker distance	Average LD
Exonic SNPs	36	26 kb	$0.65 \pm 0.021$
Non exonic SNPs	60	36 kb	$0.48 \pm 0.018$
Exonic/Non exonic	96	32 kb	$0.60 \pm 0.015$

**FIGURE 15**

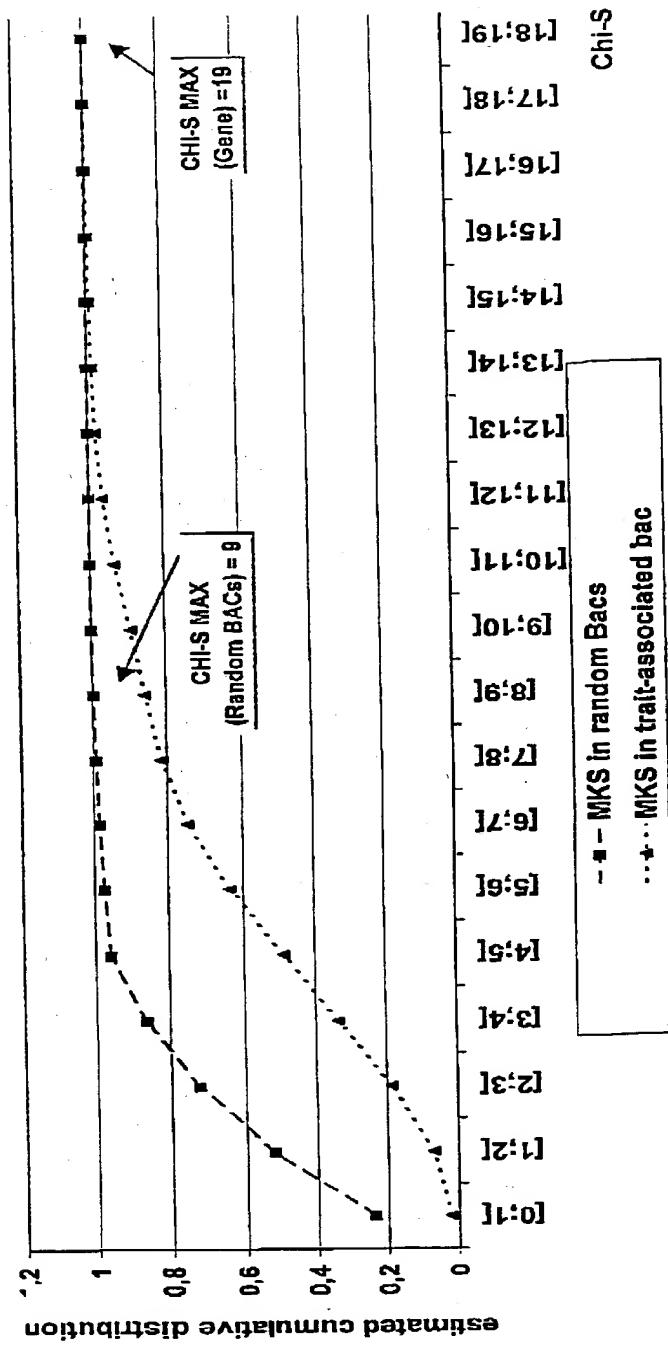


FIGURE 16 A

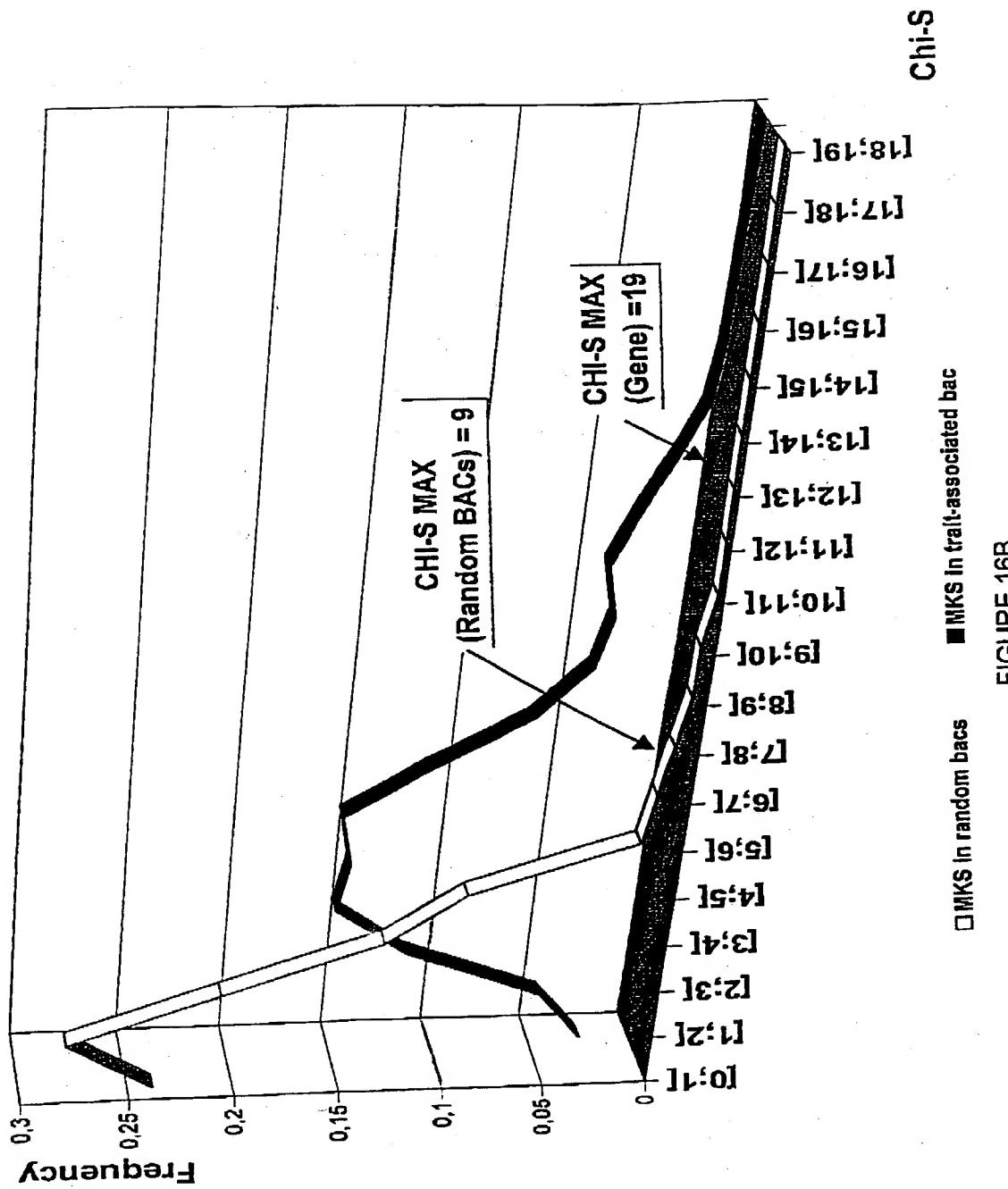


FIGURE 16B

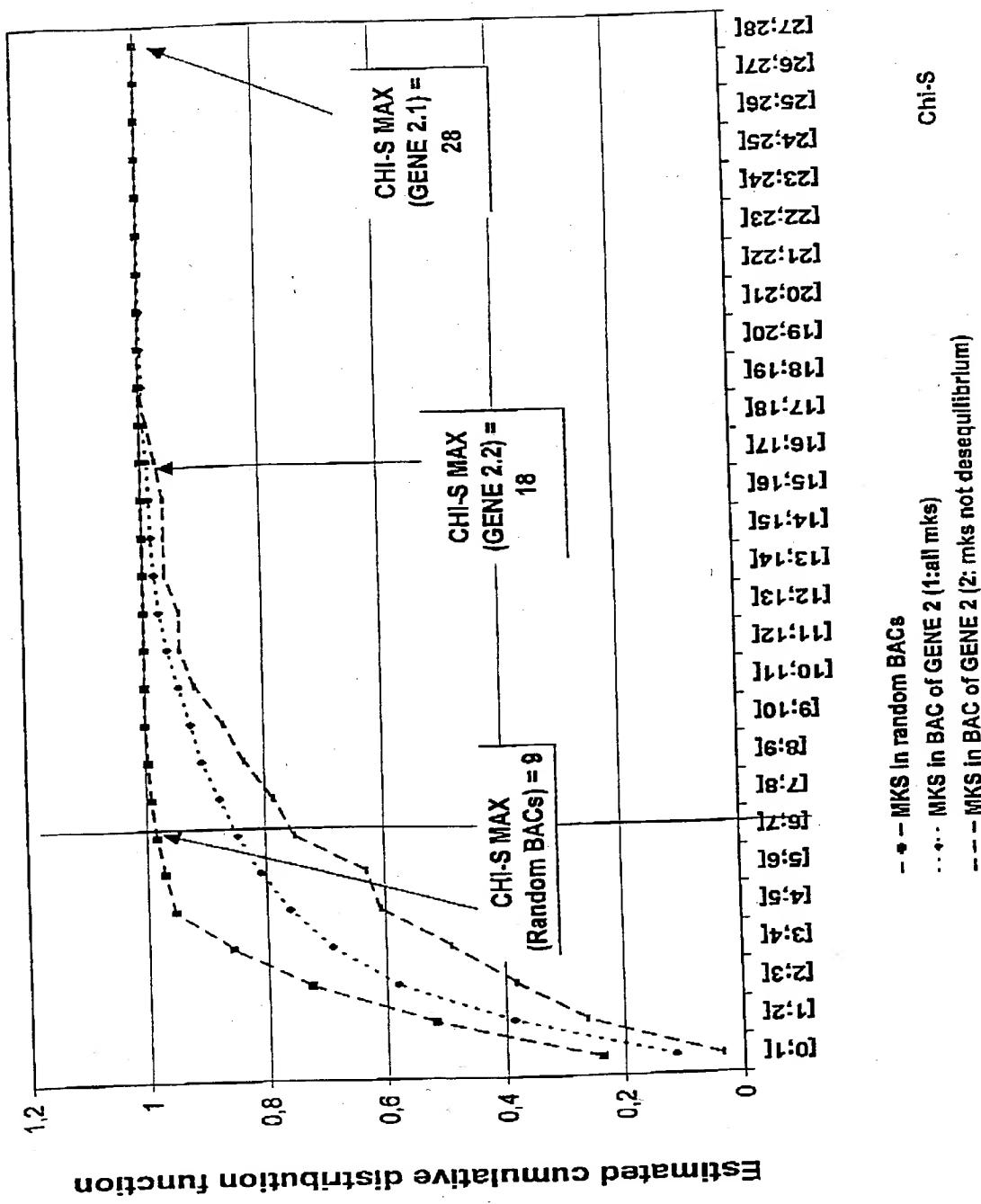


FIGURE 17A

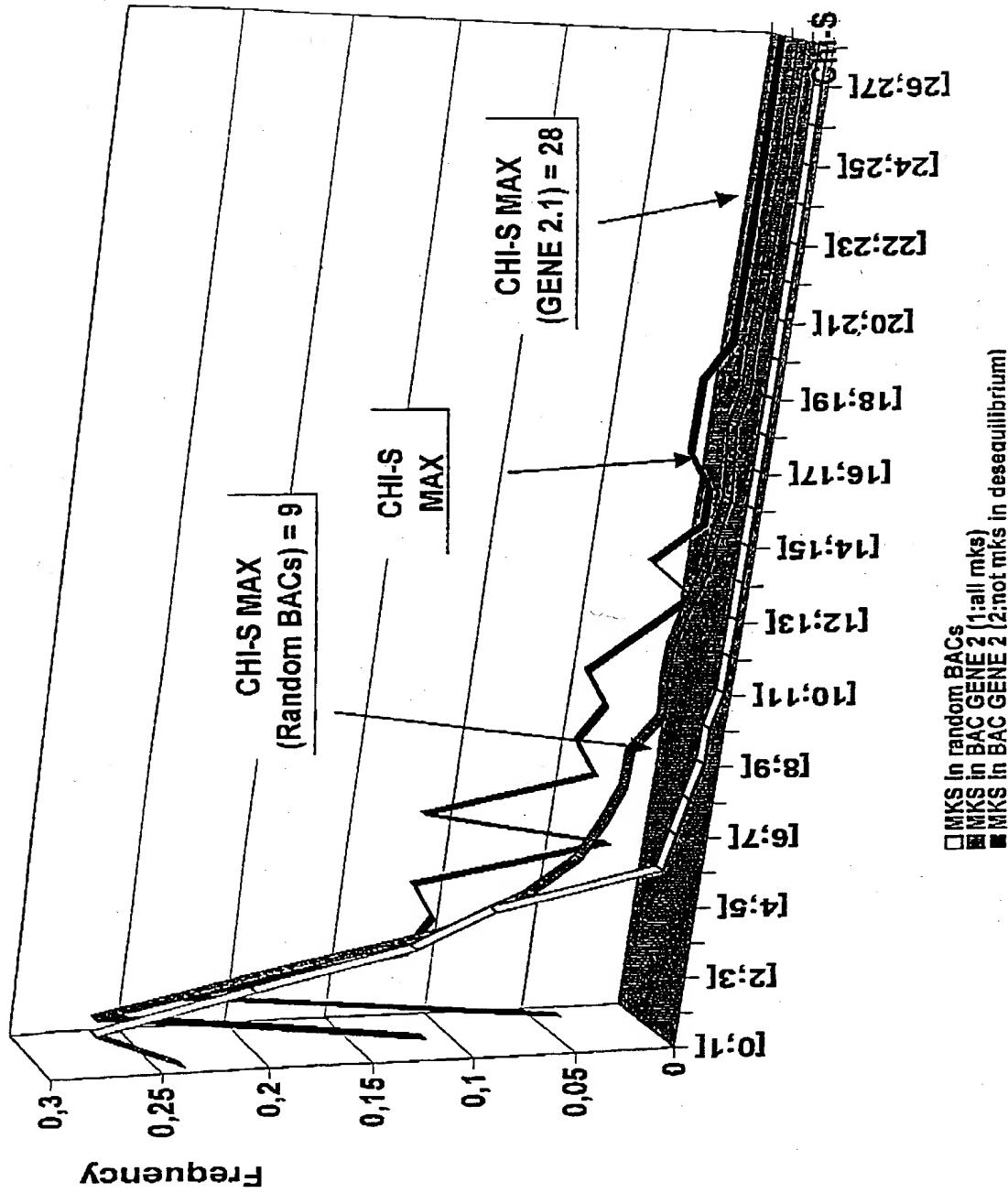


FIGURE 17 B

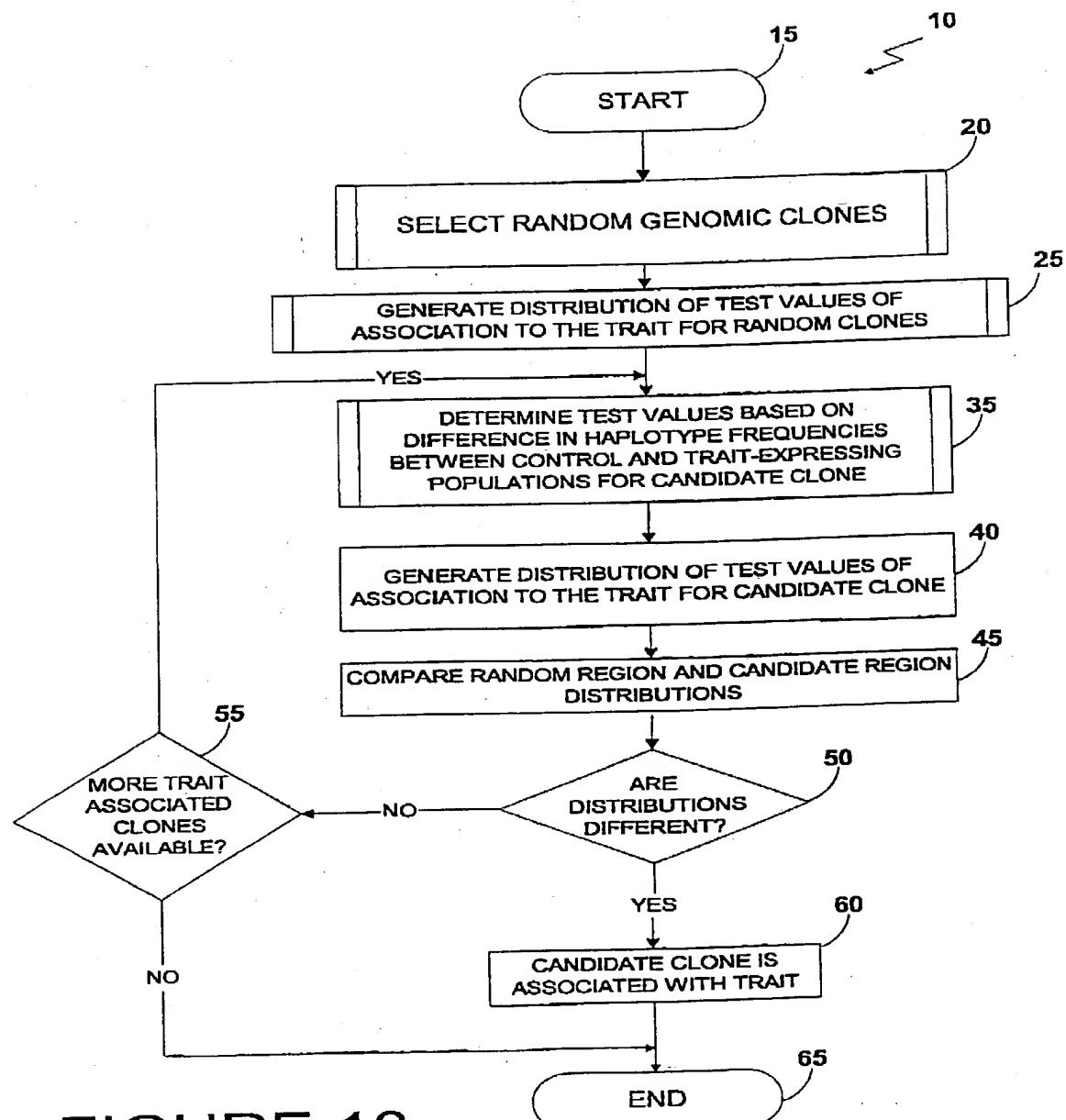


FIGURE 18

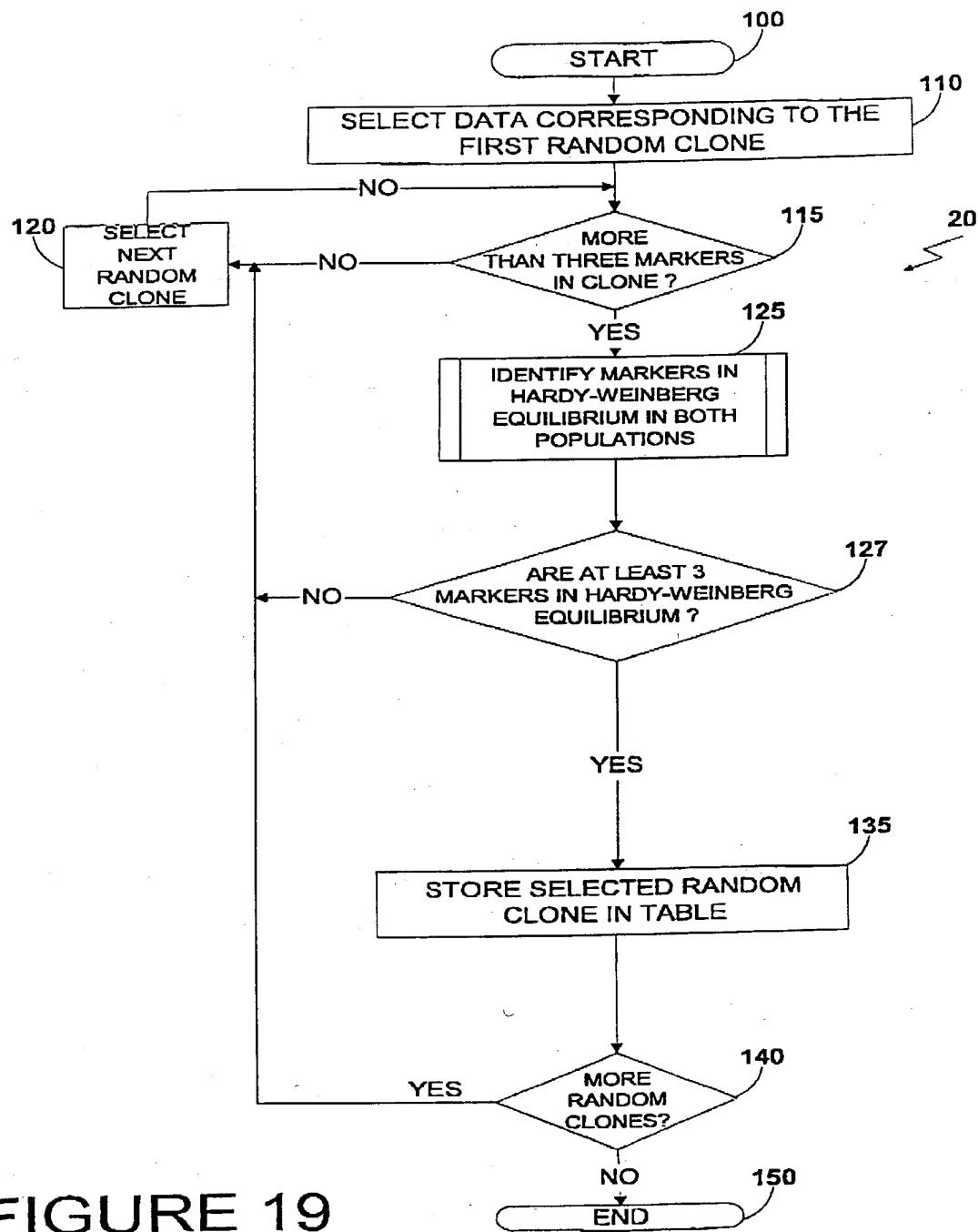


FIGURE 19

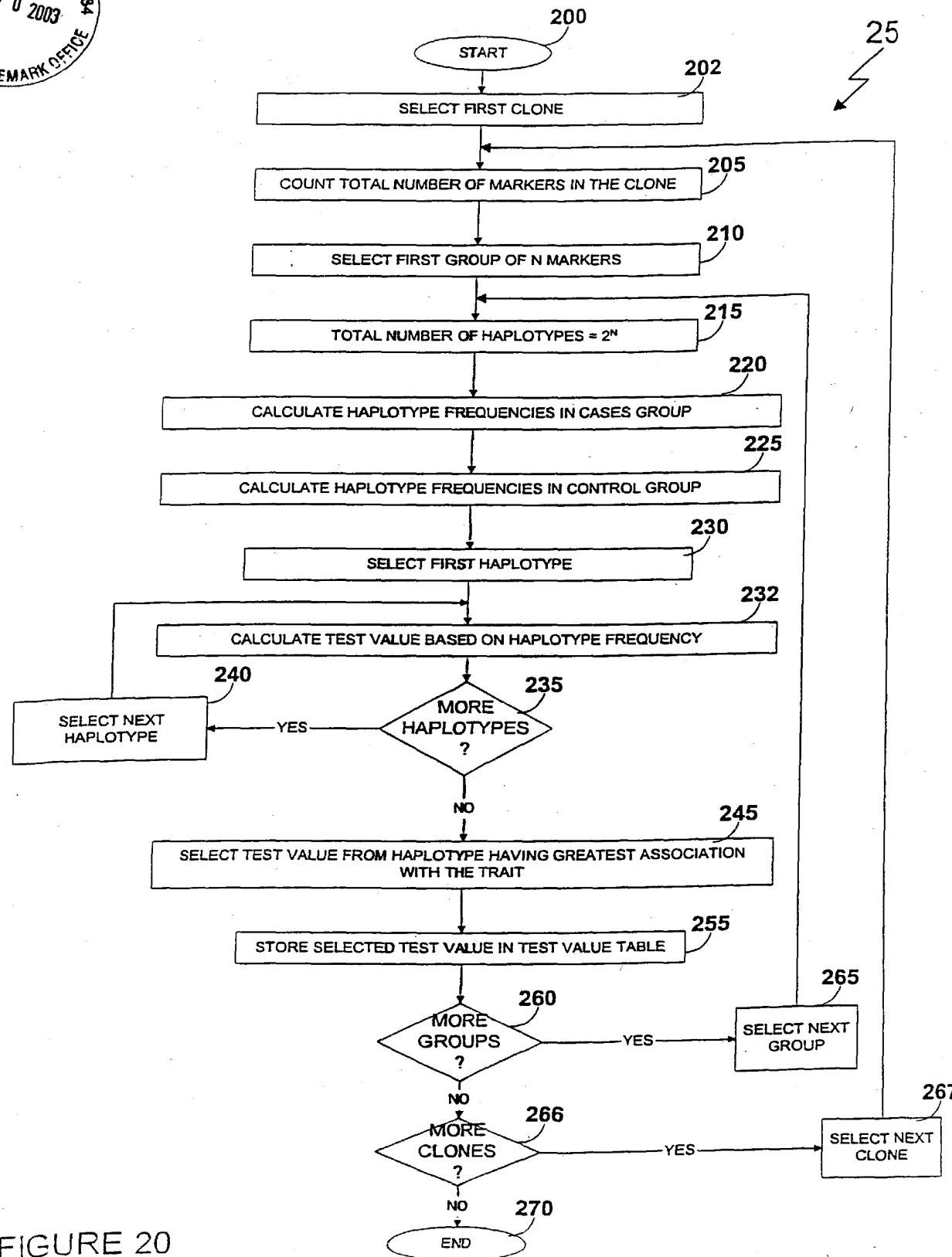


FIGURE 20

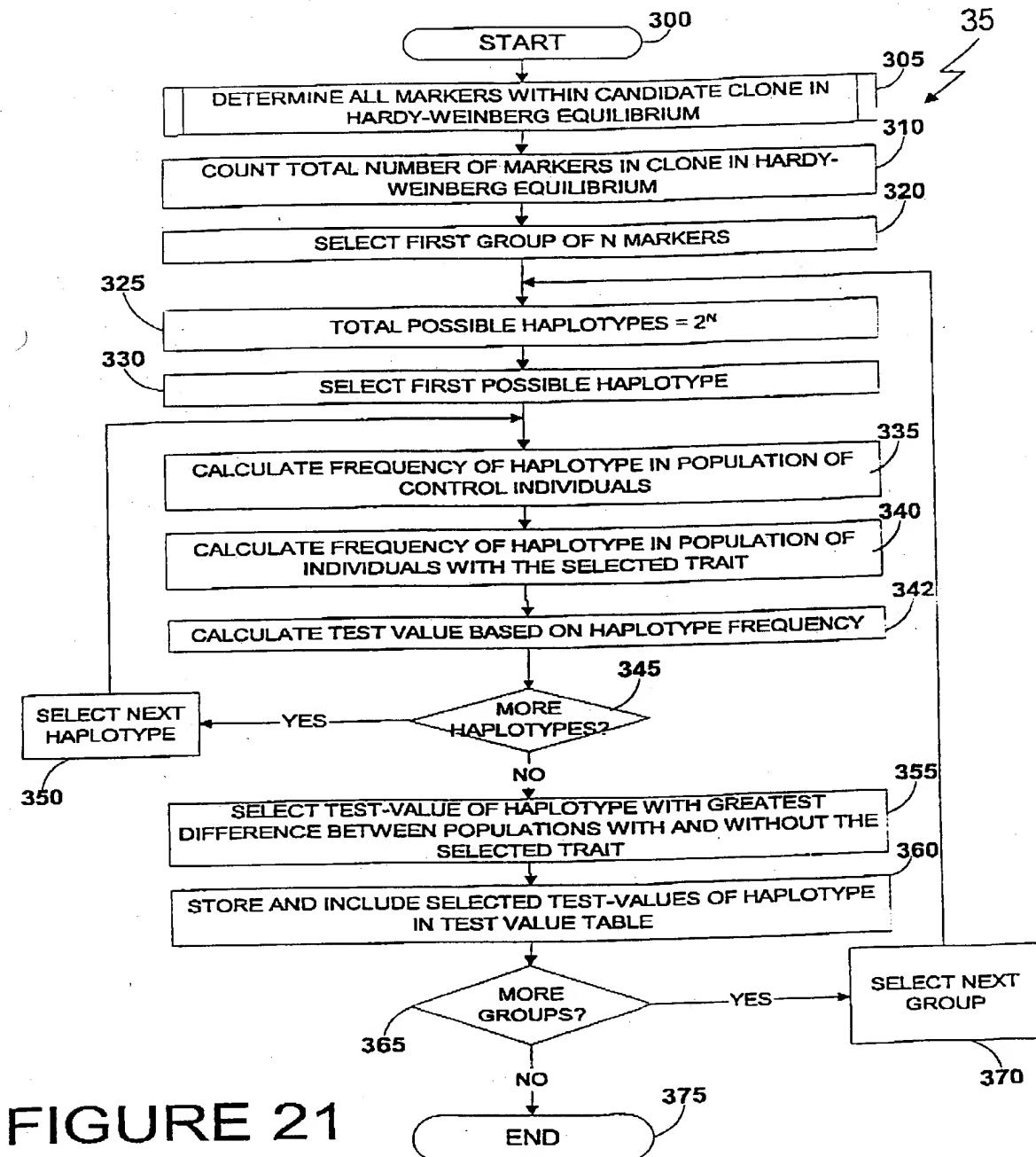


FIGURE 21

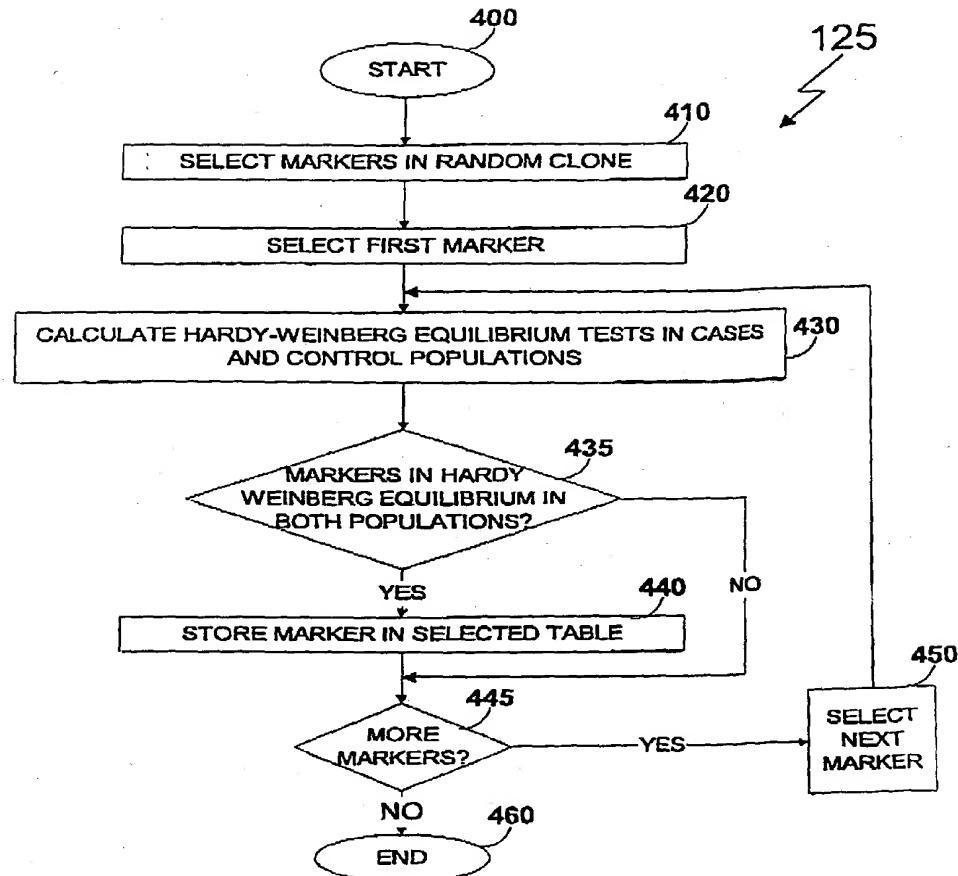


FIGURE 22

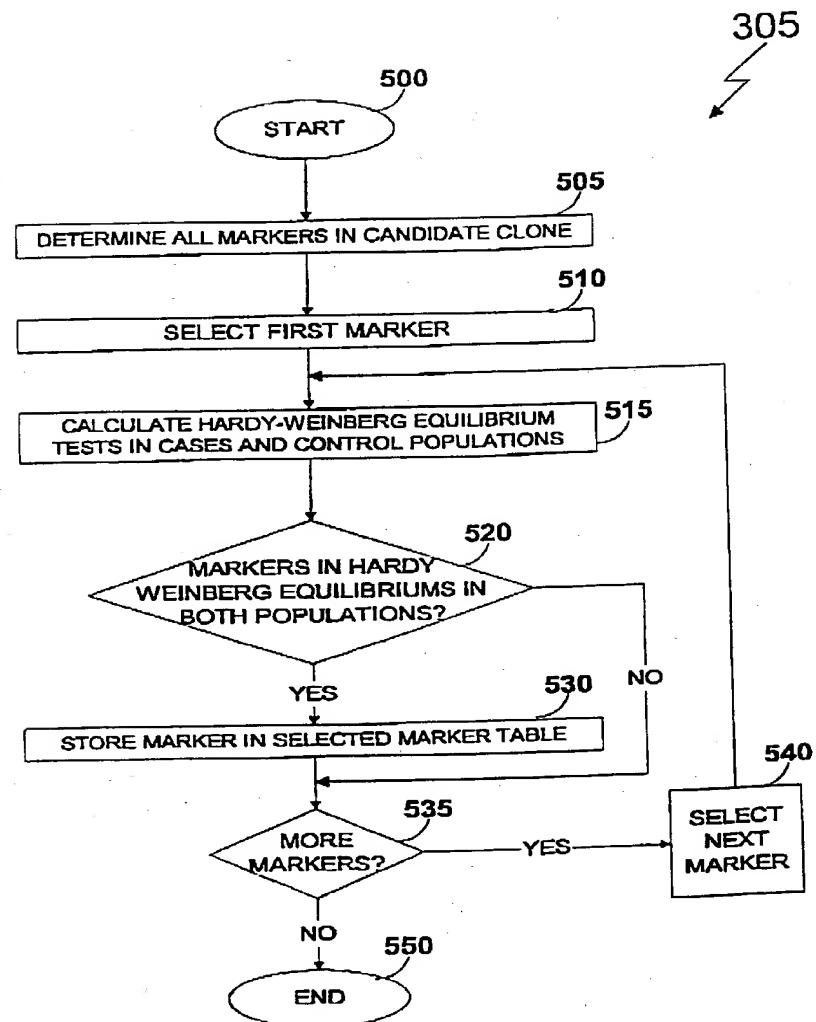


FIGURE 23

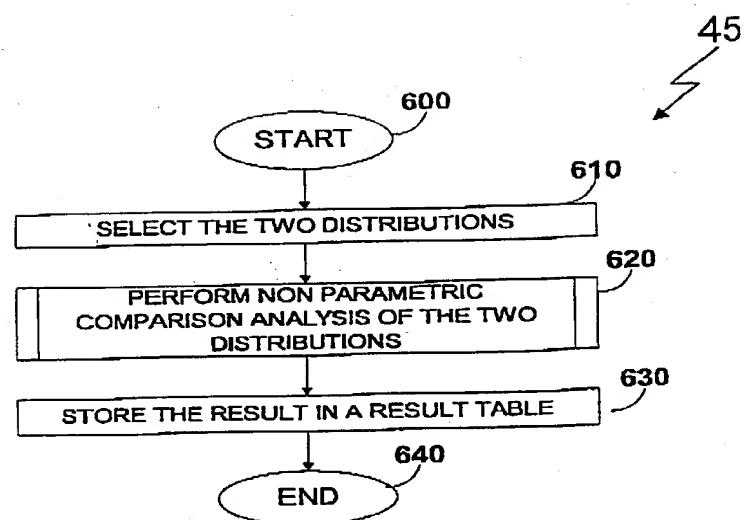


FIGURE 24

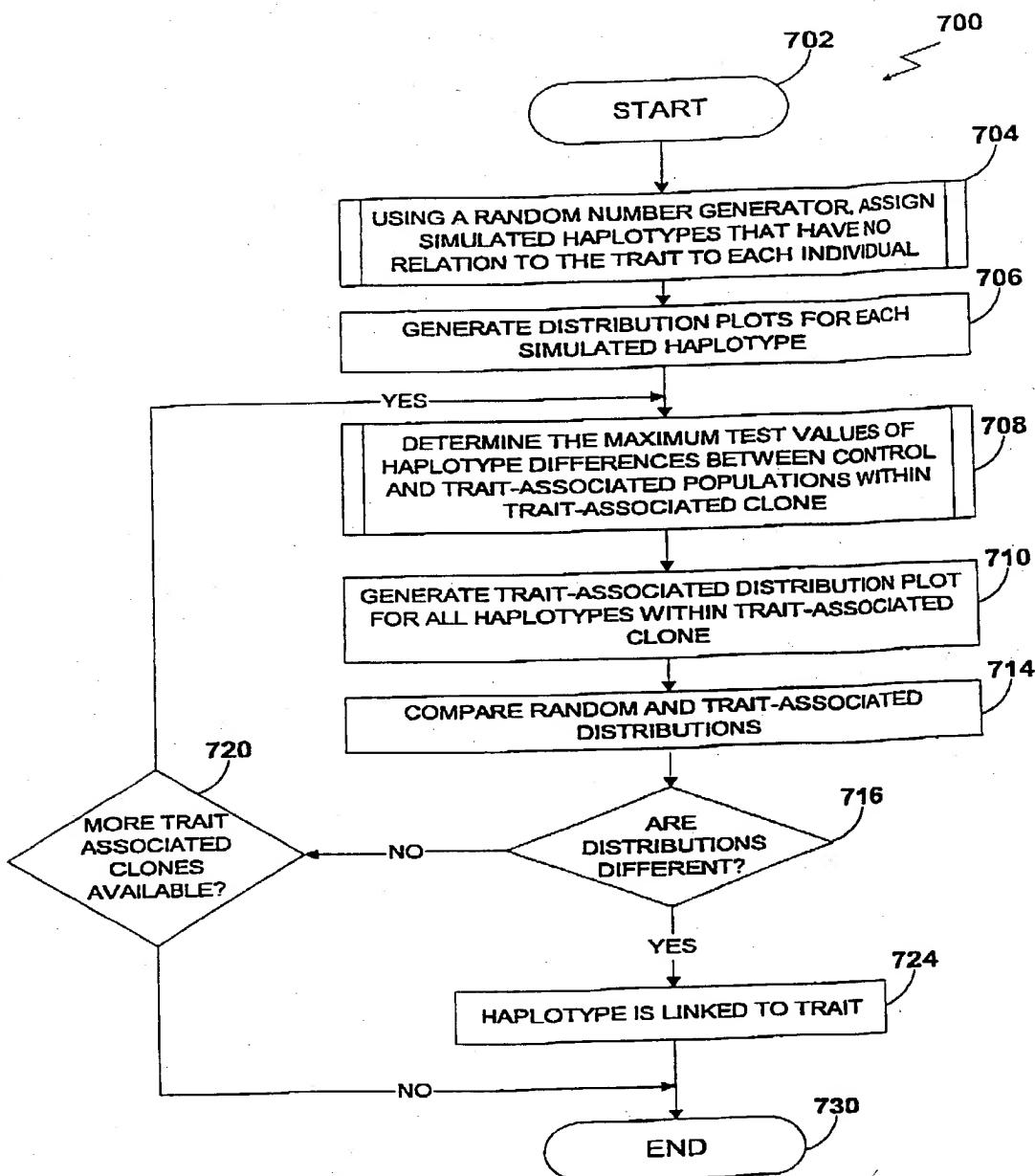
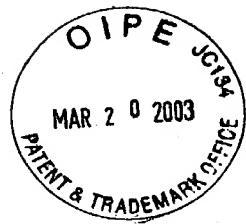


FIGURE 25